

SEQUENCE LISTING

<110> Hellström, Mats
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<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND
COMPOSITIONS, AND METHODS OF USE THEREOF

<130> 78063

<160> 52

<170> PatentIn version 3.2

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<212> DNA

<213> Murinae gen. sp.

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<212> PRT
<213> Murinae gen. sp.

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Arg	Arg	Thr	Tyr	Pro	Arg	Pro	His	Glu	Tyr	Leu	Ser	Pro	Ala	Asp	Leu
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Pro	Lys	Asn	Trp	Asp	Trp	Arg	Asn	Val	Asn	Gly	Val	Asn	Tyr	Ala	Ser
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Val	Thr	Arg	Asn	Gln	His	Ile	Pro	Gln	Tyr	Cys	Gly	Ser	Cys	Trp	Ala
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Ala Lys Asp Gln Asp Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Thr
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Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile
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Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met
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Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val
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Ile Glu Tyr Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu
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 <213> Homo sapiens

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<213> Homo sapiens

<400> 5

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Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
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Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr
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Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala
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Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn
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His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys
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Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe
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Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp
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Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala
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Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn
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Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn
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Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp
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<213> Murinae gen. sp.

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Thr	Ala	Gly	Pro	Ser	Cys	Ser	Leu	Leu	Gln	Glu	Ala	Phe	Arg	Arg	Tyr
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Tyr	Asn	Tyr	Val	Phe	Gly	Phe	Tyr	Lys	Arg	His	His	Gly	Pro	Ala	Arg
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Phe	Arg	Ala	Glu	Pro	Gln	Leu	Gln	Lys	Leu	Leu	Val	Ser	Ile	Thr	Leu
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Glu	Ser	Glu	Cys	Glu	Ser	Phe	Pro	Ser	Leu	Ser	Ser	Asp	Glu	Thr	Tyr
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Ser	Leu	Leu	Val	Gln	Glu	Pro	Val	Ala	Val	Leu	Lys	Ala	Asn	Ser	Val
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Asp	Ser	Phe	Gly	Thr	Phe	Thr	Ile	Asn	Glu	Ser	Ser	Ile	Ala	Asp	Ser
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Pro	Arg	Phe	Pro	His	Arg	Gly	Ile	Leu	Ile	Asp	Thr	Ser	Arg	His	Phe
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Leu	Pro	Val	Lys	Thr	Ile	Leu	Lys	Thr	Leu	Asp	Ala	Met	Ala	Phe	Asn
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Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr
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Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser
 305 310 315 320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu
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Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg
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Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys
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Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp
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Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val
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Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr
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Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu
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Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu
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Asn Phe Glu Gly Ser Glu Lys Gln Lys Gln Leu Val Ile Gly Gly Glu
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Thr Val Thr Asp Leu Glu Asn Ala Tyr Lys Arg Leu Ala Val His Arg
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<212> DNA
<213> Homo sapiens

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<210> 10
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<213> Homo sapiens

<400> 10

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 35 40 45

Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Leu Val Lys
 50 55 60

Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
 65 70 75 80

His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
 85 90 95

Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
 100 105 110

His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
 115 120 125

Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
 130 135 140

Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
 145 150 155 160

Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
 165 170 175

Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
 180 185 190

Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
 195 200 205

Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
 210 215 220

Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
 225 230 235 240

Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
 245 250 255

Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
 260 265 270

Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu

275					280					285					
Phe	Asp	Thr	Pro	Gly	His	Thr	Leu	Ser	Trp	Gly	Lys	Gly	Gln	Lys	Asp
	290					295					300				
Leu	Leu	Thr	Pro	Cys	Tyr	Ser	Arg	Gln	Asn	Lys	Leu	Asp	Ser	Phe	Gly
305					310					315					320
Pro	Ile	Asn	Pro	Thr	Leu	Asn	Thr	Thr	Tyr	Ser	Phe	Leu	Thr	Thr	Phe
				325					330					335	
Phe	Lys	Glu	Ile	Ser	Glu	Val	Phe	Pro	Asp	Gln	Phe	Ile	His	Leu	Gly
			340					345					350		
Gly	Asp	Glu	Val	Glu	Phe	Lys	Cys	Trp	Glu	Ser	Asn	Pro	Lys	Ile	Gln
		355					360					365			
Asp	Phe	Met	Arg	Gln	Lys	Gly	Phe	Gly	Thr	Asp	Phe	Lys	Lys	Leu	Glu
	370					375					380				
Ser	Phe	Tyr	Ile	Gln	Lys	Val	Leu	Asp	Ile	Ile	Ala	Thr	Ile	Asn	Lys
385					390					395					400
Gly	Ser	Ile	Val	Trp	Gln	Glu	Val	Phe	Asp	Asp	Lys	Ala	Lys	Leu	Ala
				405					410					415	
Pro	Gly	Thr	Ile	Val	Glu	Val	Trp	Lys	Asp	Ser	Ala	Tyr	Pro	Glu	Glu
			420					425					430		
Leu	Ser	Arg	Val	Thr	Ala	Ser	Gly	Phe	Pro	Val	Ile	Leu	Ser	Ala	Pro
		435					440					445			
Trp	Tyr	Leu	Asp	Leu	Ile	Ser	Tyr	Gly	Gln	Asp	Trp	Arg	Lys	Tyr	Tyr
	450					455					460				
Lys	Val	Glu	Pro	Leu	Asp	Phe	Gly	Gly	Thr	Gln	Lys	Gln	Lys	Gln	Leu
465					470					475					480
Phe	Ile	Gly	Gly	Glu	Ala	Cys	Leu	Trp	Gly	Glu	Tyr	Val	Asp	Ala	Thr
				485					490					495	
Asn	Leu	Thr	Pro	Arg	Leu	Trp	Pro	Arg	Ala	Ser	Ala	Val	Gly	Glu	Arg
			500					505					510		
Leu	Trp	Ser	Ser	Lys	Asp	Val	Arg	Asp	Met	Asp	Asp	Ala	Tyr	Asp	Arg
		515					520					525			

Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
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Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met
 545 550 555

<210> 11
 <211> 676
 <212> DNA
 <213> Murinae gen. sp.

<220>
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ctccatcatc gggcgccctgc tggaagtgc gggctcacgg cctgggaaga acgtgcagct
 120

gacagagaac gagatccgtg gtctgtgcct caaatcccgg gagattttcc tgagccagcc
 180

cattcttctg gagcttgagg cggccctcaa gatctgtggt gacatccatg gccagtacta
 240

tgaccttcta cggctgtttg agtatggtgg ctccctcca gagagcaact acctcttctt
 300

gggggattat gtagatcggg gcaagcagtc tttggagacc atctgcctgt tgctggccta
 360

taagatcaga taccgggaga atttctttct acttcgtggg aaccatgagt gtgccagcat
 420

caaccgcatt tatggcttct atgatgaatg caagagaaga tacaacatca aactgtggaa
 480

gacgttcact gactgcttca actgcctgcc cattgcagcc attgtggatg agaagatctt
 540

ctgctgccac gggggcctgt ctccagactt gcaatccatg gagcagatta ggcgtattat
 600

gcnngccaca gacgtgcctg accagggcct actgtgtgat ctctgtggt ctgaccctga
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 676

<210> 12
 <211> 1369

<212> DNA

<213> Murinae gen. sp.

<400> 12

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120

tgggaagaac gtgcagctga cagagaacga gatccgtggg ctgtgcctca aatcccggga
180

gattttcctg agccagccca ttcttctgga gcttgaggcg cccctcaaga tctgtggtga
240

catccatggc cagtactatg accttctacg gctgtttgag tatggtggct tccctccaga
300

gagcaactac ctcttcttgg gggattatgt agatcggggc aagcagtctt tggagaccat
360

ctgcctgttg ctggcctata agatcagata cccggagaat ttctttctac ttctgtggaa
420

ccatgagtgt gccagcatca accgcattta tggcttctat gatgaatgca agagaagata
480

caacatcaaa ctgtggaaga cgttcactga ctgcttcaac tgcctgcca ttgcagccat
540

tgtggatgag aagatcttct gctgccacgg gggcctgtct ccagacttgc aatccatgga
600

gcagattagg cgtattatgc ggcccacaga cgtgcctgac cagggcctac tgtgtgatct
660

cctgtggtct gaccctgaca aggatgttca aggctggggc gagaatgacc gtggtgtctc
720

ctttaccttt ggggctgagg tggtagccaa gttcctgcac aagcatgatt tggacctcat
780

ctgcagagca catcagggtt tagaagatgg ctatgagttc ttgccaaga gacagttggt
840

gacactcttc tcagctccca actactgtgg agagtttgac aatgctggtg ccatgatgag
900

tgtggatgag accctcatgt gttccttcca gatcctcaag cccgctgata agaataaggg
960

caagtatggg cagttcagcg gcctgaacct cggaggcggg cccatcactc caccocgcaa
1020

ttctgcaaaa gccaagaaat agcctccatg tgctgccctt ctgccccaga tcgtttgtac
1080

agaaatcatg ctgccatggg tcacactggc ctctcaggcc caccgctcac ggggaacaca
1140

cagcgttaag tgtctttcct ttatttttta aagaatcaat agcagcatct aatctcccag
1200

ggctccctcc caccagcacc tgtggtggct gcaagtggaa tcctggggcc aaggctgcag
1260

ctcagggcaa tggcagacca gattgtgggt ctccagcctt gcatggctgg cagccagatc
1320

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1369

<210> 13
<211> 330
<212> PRT
<213> Murinae gen. sp.

<400> 13

Met	Ser	Asp	Ser	Glu	Lys	Leu	Asn	Leu	Asp	Ser	Ile	Ile	Gly	Arg	Leu
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Leu	Glu	Val	Gln	Gly	Ser	Arg	Pro	Gly	Lys	Asn	Val	Gln	Leu	Thr	Glu
			20					25					30		

Asn	Glu	Ile	Arg	Gly	Leu	Cys	Leu	Lys	Ser	Arg	Glu	Ile	Phe	Leu	Ser
		35					40					45			

Gln	Pro	Ile	Leu	Leu	Glu	Leu	Glu	Ala	Pro	Leu	Lys	Ile	Cys	Gly	Asp
	50					55					60				

Ile	His	Gly	Gln	Tyr	Tyr	Asp	Leu	Leu	Arg	Leu	Phe	Glu	Tyr	Gly	Gly
65					70					75					80

Phe	Pro	Pro	Glu	Ser	Asn	Tyr	Leu	Phe	Leu	Gly	Asp	Tyr	Val	Asp	Arg
				85					90					95	

Gly	Lys	Gln	Ser	Leu	Glu	Thr	Ile	Cys	Leu	Leu	Leu	Ala	Tyr	Lys	Ile
			100					105					110		

Arg	Tyr	Pro	Glu	Asn	Phe	Phe	Leu	Leu	Arg	Gly	Asn	His	Glu	Cys	Ala
		115					120					125			

Ser	Ile	Asn	Arg	Ile	Tyr	Gly	Phe	Tyr	Asp	Glu	Cys	Lys	Arg	Arg	Tyr
	130					135					140				

Asn	Ile	Lys	Leu	Trp	Lys	Thr	Phe	Thr	Asp	Cys	Phe	Asn	Cys	Leu	Pro
145					150					155					160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu

	165		170		175										
Ser	Pro	Asp	Leu	Gln	Ser	Met	Glu	Gln	Ile	Arg	Arg	Ile	Met	Arg	Pro
			180					185					190		
Thr	Asp	Val	Pro	Asp	Gln	Gly	Leu	Leu	Cys	Asp	Leu	Leu	Trp	Ser	Asp
		195					200					205			
Pro	Asp	Lys	Asp	Val	Gln	Gly	Trp	Gly	Glu	Asn	Asp	Arg	Gly	Val	Ser
	210					215					220				
Phe	Thr	Phe	Gly	Ala	Glu	Val	Val	Ala	Lys	Phe	Leu	His	Lys	His	Asp
225					230					235					240
Leu	Asp	Leu	Ile	Cys	Arg	Ala	His	Gln	Val	Val	Glu	Asp	Gly	Tyr	Glu
				245					250					255	
Phe	Phe	Ala	Lys	Arg	Gln	Leu	Val	Thr	Leu	Phe	Ser	Ala	Pro	Asn	Tyr
			260					265					270		
Cys	Gly	Glu	Phe	Asp	Asn	Ala	Gly	Ala	Met	Met	Ser	Val	Asp	Glu	Thr
		275					280					285			
Leu	Met	Cys	Ser	Phe	Gln	Ile	Leu	Lys	Pro	Ala	Asp	Lys	Asn	Lys	Gly
	290					295					300				
Lys	Tyr	Gly	Gln	Phe	Ser	Gly	Leu	Asn	Pro	Gly	Gly	Arg	Pro	Ile	Thr
305					310					315					320
Pro	Pro	Arg	Asn	Ser	Ala	Lys	Ala	Lys	Lys						
				325					330						

<210> 14
 <211> 993
 <212> DNA
 <213> Homo sapiens

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 120
 aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag
 180
 atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt
 240

ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc
300

ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg
360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc
420

aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc
480

atcgcgcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg
540

cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg
600

ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac
660

cgtggcgtct cttttacctt tggagccgag gtgggtggcca agttcctcca caagcacgac
720

ttggacctca tctgccgagc acaccagggtg gtagaagacg gctacgagtt ctttgccaag
780

cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc
840

gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac
900

aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc
960

ccaccccgca attccgcca agccaagaaa tag
993

<210> 15

<211> 330

<212> PRT

<213> Homo sapiens

<400> 15

Met	Ser	Asp	Ser	Glu	Lys	Leu	Asn	Leu	Asp	Ser	Ile	Ile	Gly	Arg	Leu
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Leu	Glu	Val	Gln	Gly	Ser	Arg	Pro	Gly	Lys	Asn	Val	Gln	Leu	Thr	Glu
			20					25					30		

Asn	Glu	Ile	Arg	Gly	Leu	Cys	Leu	Lys	Ser	Arg	Glu	Ile	Phe	Leu	Ser
		35					40					45			

Gln	Pro	Ile	Leu	Leu	Glu	Leu	Glu	Ala	Pro	Leu	Lys	Ile	Cys	Gly	Asp
	50					55					60				

Ile	His	Gly	Gln	Tyr	Tyr	Asp	Leu	Leu	Arg	Leu	Phe	Glu	Tyr	Gly	Gly	65	70	75	80
Phe	Pro	Pro	Glu	Ser	Asn	Tyr	Leu	Phe	Leu	Gly	Asp	Tyr	Val	Asp	Arg	85	90	95	
Gly	Lys	Gln	Ser	Leu	Glu	Thr	Ile	Cys	Leu	Leu	Leu	Ala	Tyr	Lys	Ile	100	105	110	
Lys	Tyr	Pro	Glu	Asn	Phe	Phe	Leu	Leu	Arg	Gly	Asn	His	Glu	Cys	Ala	115	120	125	
Ser	Ile	Asn	Arg	Ile	Tyr	Gly	Phe	Tyr	Asp	Glu	Cys	Lys	Arg	Arg	Tyr	130	135	140	
Asn	Ile	Lys	Leu	Trp	Lys	Thr	Phe	Thr	Asp	Cys	Phe	Asn	Cys	Leu	Pro	145	150	155	160
Ile	Ala	Ala	Ile	Val	Asp	Glu	Lys	Ile	Phe	Cys	Cys	His	Gly	Gly	Leu	165	170	175	
Ser	Pro	Asp	Leu	Gln	Ser	Met	Glu	Gln	Ile	Arg	Arg	Ile	Met	Arg	Pro	180	185	190	
Thr	Asp	Val	Pro	Asp	Gln	Gly	Leu	Leu	Cys	Asp	Leu	Leu	Trp	Ser	Asp	195	200	205	
Pro	Asp	Lys	Asp	Val	Gln	Gly	Trp	Gly	Glu	Asn	Asp	Arg	Gly	Val	Ser	210	215	220	
Phe	Thr	Phe	Gly	Ala	Glu	Val	Val	Ala	Lys	Phe	Leu	His	Lys	His	Asp	225	230	235	240
Leu	Asp	Leu	Ile	Cys	Arg	Ala	His	Gln	Val	Val	Glu	Asp	Gly	Tyr	Glu	245	250	255	
Phe	Phe	Ala	Lys	Arg	Gln	Leu	Val	Thr	Leu	Phe	Ser	Ala	Pro	Asn	Tyr	260	265	270	
Cys	Gly	Glu	Phe	Asp	Asn	Ala	Gly	Ala	Met	Met	Ser	Val	Asp	Glu	Thr	275	280	285	
Leu	Met	Cys	Ser	Phe	Gln	Ile	Leu	Lys	Pro	Ala	Asp	Lys	Asn	Lys	Gly	290	295	300	

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
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Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
325 330

<210> 16
<211> 702
<212> DNA
<213> Murinae gen. sp.

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120
tctcagctat cacagcctta cagcaaagcc actatctctt tggattttga aattttctct
180
gccatgccta tgactatttt aaaattgggc aaagtatatc catttcagag gggctttttc
240
tgtactgaca acagcgtgaa gtacccgtac catgacagta ccatcccgtc ccgtatactc
300
gccatactgg ggcttggctt acccattttc tctatgagta tggagaatct ctgtctgttt
360
actttaatgt cttgcattcg aattcctttg tcggcaatcc ctacatagcc accatttaca
420
aagccgtcgg agccttttgt tcggagtctc agctagtcag tccttgactg acatcgctaa
480
gtatactata ggcagtttgc ggccgcactt cttggctatc tgtaaccag actggtcaaa
540
aatcaactgc agtgatggct atattgagga ctacatatgt caagggaatg aagagaaagt
600
caaggagggc aggttgtctt tctactcggg aactcttca ttctctatgt actgcatgct
660
gtttgtcgca ctttatcttc aagccaggat gaagggagac tg
702

<210> 17
<211> 1432
<212> DNA
<213> Murinae gen. sp.

<400> 17
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120

gcagggcggc ccaatccaaa ctgccctggg ccttgctccc gtcagtctaa gaggctcgca
180

gtcgcttggg gcggccgcca tcccaggggc ggggctctgg gaattgggta tctggaccgc
240

cgcggtctgt tcctcccgcc actcgcacca ggtggtgaca ccatccagcc ggtgaccatg
300

ttcgacaaga cgcggctgcc gtacgtggcc ctcgatgtga tttgcgtggt gctggctgga
360

ttgccttttg caattcttac ttcaaggcat acccccttcc agcgaggaat attctgtaat
420

gatgactcca tcaagtaccc ttacaaggaa gacaccatac cttatgcctt attaggtgga
480

atagtcattc cattctgtat tatcgttatg agtattggag aatctctgtc tgtttacttt
540

aatgtcttgc attcgaattc ctttgtcggc aatccctaca tagccaccat ttacaaagcc
600

gtcggagcct ttttgttcgg agtctcagct agtcagtcct tgactgacat cgctaagtat
660

actataggca gtttgcggcc gcacttcttg gctatctgta acccagactg gtcaaaaatc
720

aactgcagtg atggctatat tgaggactac atatgtcaag ggaatgaaga gaaagtcaag
780

gagggcaggt tgtctttcta ctcgggacac tcttcattct ctatgtactg catgctgttt
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gtcgcacttt atcttcaagc caggatgaag ggagactggg caagactctt acgacccatg
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960

aaacaccact ggagtgaagt cacagttgga ctcatcagg gagctgctat ggctatactg
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gttgctttgt atgtatccga tttcttcaag gacacacatt cttacaaaga gagaaaggaa
1080

gaggatccac acacgactct ccatgaaacc gccagttcac ggaactactg ggcgctggcc
1140

cgcttcaaag gcaacagctg gaggctaaag gcagggggat gcgtattact tcctgctgta
1200

cagaccattc tataaaggac tgctgctatc tatacctcct ggatgcccac tttatgtgtg
1260

tacagttact tctaacacaa tgagtaacag ttcaattaaa gaaaatgaag cctgtcacta
1320

aaacactgtc ccacctgtac atttttattg aaagacgcta tgtacaaatg tgtatgttac
1380

atgccttctc agaatgatgt tgacttaaata ataataaaaa gcttgtgaac ca
1432

<210> 18

<211> 378

<212> PRT

<213> Murinae gen. sp.

<400> 18

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Arg Pro Asn Pro Asn Cys Pro Gly Pro Cys Ser Arg Gln Ser Lys Arg
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Leu Ala Val Ala Trp Gly Gly Arg His Pro Glu Gly Gly Ala Leu Gly
35 40 45

Ile Gly Tyr Leu Asp Arg Arg Gly Leu Phe Leu Pro Pro Leu Ala Pro
50 55 60

Gly Gly Asp Thr Ile Gln Pro Val Thr Met Phe Asp Lys Thr Arg Leu
65 70 75 80

Pro Tyr Val Ala Leu Asp Val Ile Cys Val Leu Leu Ala Gly Leu Pro
85 90 95

Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg Gly Ile Phe
100 105 110

Cys Asn Asp Asp Ser Ile Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro
115 120 125

Tyr Ala Leu Leu Gly Gly Ile Val Ile Pro Phe Cys Ile Ile Val Met
130 135 140

Ser Ile Gly Glu Ser Leu Ser Val Tyr Phe Asn Val Leu His Ser Asn
145 150 155 160

Ser Phe Val Gly Asn Pro Tyr Ile Ala Thr Ile Tyr Lys Ala Val Gly
165 170 175

Ala Phe Leu Phe Gly Val Ser Ala Ser Gln Ser Leu Thr Asp Ile Ala
180 185 190

Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu Ala Ile Cys Asn
195 200 205

Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Asp Tyr
210 215 220

Ile Cys Gln Gly Asn Glu Glu Lys Val Lys Glu Gly Arg Leu Ser Phe
225 230 235 240

Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala
245 250 255

Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg
260 265 270

Pro Met Leu Gln Phe Gly Leu Ile Ala Phe Ser Ile Tyr Val Gly Leu
275 280 285

Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Thr Val Gly
290 295 300

Leu Ile Gln Gly Ala Ala Met Ala Ile Leu Val Ala Leu Tyr Val Ser
305 310 315 320

Asp Phe Phe Lys Asp Thr His Ser Tyr Lys Glu Arg Lys Glu Glu Asp
325 330 335

Pro His Thr Thr Leu His Glu Thr Ala Ser Ser Arg Asn Tyr Trp Ala
340 345 350

Leu Ala Arg Phe Lys Gly Asn Ser Trp Arg Leu Lys Ala Gly Gly Cys
355 360 365

Val Leu Leu Pro Ala Val Gln Thr Ile Leu
370 375

<210> 19
<211> 1626
<212> DNA
<213> Homo sapiens

<400> 19
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120

caggccgtgc cggctgagga ggtcctgagg ctacagagct gccgcggctg gcacacgagc
180

gcctcggcac taaccgagtg ttgcgcgggg ctgtgagggg agggccccgg gcgccattgc
240

tggcgggtgg agcgccgccc ggtctcagcc cgccctcggc tgctctcttc ctccggctgg
300

gaggggccgt agctcggggc cgtcgccagc cccggccccg gctcgagaat caagggcctc
360

ggccgcccgt ccgcagctca gtccatcgcc cttgccgggc agcccgggca gagaccatgt
420

ttgacaagac gcggctgccg tacgtggccc tcgatgtgct ctgcgtgttg ctggcttcca
480

tgcctatggc tgttctaaaa ttggggccaaa tatatccatt tcagagaggg tttttctgta
540

aagacaacag catcaactat ccgtaccatg acagtaccgt cacatccact gtcctcatcc
600

tagtgggggt tggcttgccc atttcctcta ttattcttgg agaaaccctg tctgtttact
660

gtaacctttt gcactcaaatt tcctttatca ggaataacta catagccact atttaciaag
720

ccattggaac ctttttatatt ggtgcagctg ctagtcagtc cctgactgac attgccaagt
780

attcaatagg cagactgcgg cctcacttct tggatgtttg tgatccagat tgggtcaaaaa
840

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900

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960

ttgtggcact ttatcttcaa gccaggatga agggagactg ggcaagactc ttacgcccc
1020

cactgcaatt tgggtcttgtt gccgtatcca tttatgtggg cctttctcga gtttctgatt
1080

ataaacacca ctggagcgat gtgttgactg gactcattca gggagctctg gttgcaatat
1140

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1200

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1260

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1320

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1380

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1440

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1500

gccccacctg tatacatctt tattaaaaaa atgtaatgct tatgtataaa catgtatgta
1560

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1620

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1626

<210> 20
<211> 378
<212> PRT
<213> Homo sapiens

<400> 20

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Pro Leu Leu Ala Val Gly Ala Pro Pro Gly Leu Ser Pro Pro Ser Ala
35 40 45

Ala Leu Leu Leu Arg Leu Gly Gly Ala Val Ala Arg Gly Arg Arg Gln
50 55 60

Pro Arg Pro Gly Leu Glu Asn Gln Gly Pro Arg Pro Pro Ser Arg Ser
65 70 75 80

Ser Val His Arg Pro Cys Arg Ala Ala Arg Ala Glu Thr Met Phe Asp
85 90 95

Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu
100 105 110

Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe
115 120 125

Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His
 130 135 140

Asp Ser Thr Val Thr Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu
 145 150 155 160

Pro Ile Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn
 165 170 175

Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile
 180 185 190

Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser
 195 200 205

Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe
 210 215 220

Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly
 225 230 235 240

Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu
 245 250 255

Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys
 260 265 270

Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp
 275 280 285

Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser
 290 295 300

Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser
 305 310 315 320

Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val
 325 330 335

Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu
 340 345 350

Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr
 355 360 365

Gly Asn His Tyr Pro Ser Asn His Gln Pro

370

375

<210> 21
<211> 816
<212> DNA
<213> Homo sapiens

<400> 21
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120
ataccttatg cgttattagg tgggaataatc attccattca gtattatcgt tattattctt
180
ggagaaacc tgtctgttta ctgtaacctt ttgcactcaa attcctttat caggaataac
240
tacatagcca ctatttacaagccattgga accttttttat ttggtgcagc tgctagtcag
300
tccctgactg acattgccaa gtattcaata ggcagactgc ggcctcactt cttggatggt
360
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420
cgagggaatg cagaaagagt taaggaaggc aggttgtcct tctattcagg ccactcttcg
480
ttttccatgt actgcatgct gtttgtggca ctttatcttc aagccaggat gaaggagac
540
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600
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660
caggagctc tggttgcaat attagttgct gtatatgtat cggatttctt caaagaaaga
720
acttctttta aagaaagaaa agaggaggac tctcatacaa ctctgcatga aacaccaaca
780
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816

<210> 22
<211> 271
<212> PRT
<213> Homo sapiens

<400> 22

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Lys	Tyr	Pro	Tyr	Lys	Glu	Asp	Thr	Ile	Pro	Tyr	Ala	Leu	Leu	Gly	Gly	35	40	45
Ile	Ile	Ile	Pro	Phe	Ser	Ile	Ile	Val	Ile	Ile	Leu	Gly	Glu	Thr	Leu	50	55	60
Ser	Val	Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arg	Asn	Asn	65	70	75
Tyr	Ile	Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	85	90	95
Ala	Ala	Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	100	105	110
Leu	Arg	Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	115	120	125
Asn	Cys	Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	130	135	140
Glu	Arg	Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	145	150	155
Phe	Ser	Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	165	170	175
Met	Lys	Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	180	185	190
Leu	Val	Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	195	200	205
Lys	His	His	Trp	Ser	Asp	Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	210	215	220
Val	Ala	Ile	Leu	Val	Ala	Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	225	230	235
Thr	Ser	Phe	Lys	Glu	Arg	Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	245	250	255

Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
260 265 270

<210> 23
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<212> DNA
<213> Murinae gen. sp.

<220>
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<400> 23
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120

agtacagggg cctgggtgcgc aaaggggaaga aaagcaaaag acgaaaatgg ctaaatttaa
180

gatccgtcca gccactgcct ctgactgcag tgacatcctg cgactgatca aggaactggc
240

taaatatgaa tacatggaag atcaagtcac tttaactgag aaagatctcc aagaggatgg
300

ctttggagaa cacccttct accactgcct ggttgcagaa gtgcctaaag agcactggac
360

ccctgaagga catagcattg ttgggttcgc catgtactat ttacctatg acccatggat
420

tggcaagttg ctgtatcttg aagacttctt cgtgatgagt gattacagag gctntggat
480

aggatcagaa attttgaaga atctaagcca gggtgccatg aagtgtcgct gcagcagtat
540

gcacttcttg gtagcagaat ggaatgaacc atctatcaac ttctacaaaa gaagaggtgc
600

ttcggatctg tccagtgaag agggatggga ggctcttcaa gattgacaag agtacttgct
660

aaaaatggca gcagaggagt gaggcgtgcc ggtgtagaac atgacaacct ccattgtgct
720

ttagaataat tctcagcttc ccttgcttct tatcttgtgg ttaggtgaa ataataagac
780

gagccaccat tccaaagctt tattaccagt gacgtgttgc atgtttgaaa tcggtctggt
840

<210> 24

<211> 1052
<212> DNA
<213> Murinae gen. sp.

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120
cctcctgctg ttcaagtaca ggggcctggg gcgcaaaggg aagaaaagca aaagacgaaa
180
atggctaaat ttaagatccg tccagccact gcctctgact gcagtgcacat cctgcgactg
240
atcaaggaac tggctaaata tgaatacatg gaagatcaag tcatttttaac tgagaaagat
300
ctccaagagg atggcttttg agaacacccc ttctaccact gcctgggtgc agaagtgcct
360
aaagagcact ggaccctga aggacatagc attggtgggt tcgccatgta ctattttacc
420
tatgacccat ggattggcaa gttgctgtat cttgaagact tcttcgtgat gaggattac
480
agaggctttg gtataggatc agaaattttg aagaatctaa gccagggtgc catgaagtgt
540
cgctgcagca gtatgcactt cttggtagca gaatggaatg aaccatctat caacttctac
600
aaaagaagag gtgcttcgga tctgtccagt gaagagggat ggaggctctt caagattgac
660
aaagagtact tgctaaaaat ggcagcagag gaggtaggag tgccgggtgta gacaatgaca
720
acctccattg tgcttttagaa taattctcag cttcccttgc tttctatctt gtgtgtagtg
780
aaataataga gcgagcacc attccaaagc ttattacca gtgacgttgt tgcattgttg
840
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900
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1020
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1052

<210> 25

<211> 171
<212> PRT
<213> Murinae gen. sp.

<400> 25

Met Ala Lys Phe Lys Ile Arg Pro Ala Thr Ala Ser Asp Cys Ser Asp
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Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met Glu Asp
20 25 30

Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu
35 40 45

His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp
50 55 60

Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr
65 70 75 80

Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val
85 90 95

Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn
100 105 110

Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu
115 120 125

Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly
130 135 140

Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp
145 150 155 160

Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu
165 170

<210> 26
<211> 1111
<212> DNA
<213> Homo sapiens

<400> 26

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120

ctcctactgt tcaagtacag gggcctggtc cgcaaaggga agaaaagcaa aagacgaaaa
180

tggctaaatt cgtgatccgc ccagccactg ccgccgactg cagtgcata ctgcggctga
240

tcaaggagct ggctaaatat gaatacatgg aagaacaagt aatcttaact gaaaaagatc
300

tgctagaaga tggtttttga gagcaccctt tttaccactg cctggttgca gaagtgccga
360

aagagcactg gactccggaa ggtaaccctt cgccctttcc agaagccaga gagaccaaca
420

ttgttggttt tgccatgtac tattttacct atgaccctg gattggcaag ttattgtatc
480

ttgaggactt cttcgtgatg agtgattata gaggtacgat tgagctttgg cataggatca
540

gaaattctga agaataaag ccagggtgca atgaggtgct gctggcagca tgcacttctt
600

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660

ccagtgaaga gggttggaga ctgttcaaga tcgacaagga gtacttgcta aaaatggcaa
720

cagaggagtg aggagtgctg ctgtagatga caacctccat tctatttttag aataaattcc
780

caacttctct tgctttctat gctgtttgta gtgaaataat agaataagca cccattccaa
840

agctttatta ccagtggcgt tggtgcatgt ttgaaatgag gtctgtttta agtggcaatc
900

tcagatgcag tttggagagt cagatctttc tccttgaata tctttogata aacaacaagg
960

tgggtgatc ttaatatatt tgaaaaaac ttcattctcg tgagtcattt aaatgtgtac
1020

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1080

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<210> 27

<211> 190

<212> PRT

<213> Homo sapiens

<400> 27

Glu Pro Pro Pro Pro Thr Val Gln Val Gln Gly Pro Gly Pro Gln Arg

1

5

10

15

Glu Glu Lys Gln Lys Thr Lys Met Ala Lys Phe Val Ile Arg Pro Ala
20 25 30

Thr Ala Ala Asp Cys Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu Ala
35 40 45

Lys Tyr Glu Tyr Met Glu Glu Gln Val Ile Leu Thr Glu Lys Asp Leu
50 55 60

Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Val Ala
65 70 75 80

Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly Asn Pro Ser Pro Phe
85 90 95

Pro Glu Ala Arg Glu Thr Asn Ile Val Gly Phe Ala Met Tyr Tyr Phe
100 105 110

Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe
115 120 125

Val Met Ser Asp Tyr Arg Gly Thr Ile Glu Leu Trp His Arg Ile Arg
130 135 140

Asn Ser Glu Glu Ser Lys Pro Gly Cys Asn Glu Val Ser Leu Ala Ala
145 150 155 160

Cys Thr Ser Trp Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys
165 170 175

Arg Arg Gly Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg
180 185 190

<210> 28

<211> 745

<212> DNA

<213> Murinae gen. sp.

<400> 28

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120

agaggagtgt ccttcacatt tgggtgcagaa gtgggttgcaa aatttctcca taagcatgat
180

tcggatctta tatgtagagc ccatcaggtg gttgaagatg gctatgagtt tttcgcaaag
240

aggcagttag tcactctggt gttctgcgag cccaactact gtggcgagtt tgacaatgca
300

ggcgccatga tgagtgtgga tgagaccctc atgtgttcct tccagatttt aaagcctgca
360

gagaaaaaga agcccaacgc cacgagacct gtcacaccac cacgggggtat gatcaciaag
420

caagcaaaga aatagatgtc acttgacact gcctgggttg gacttgtaac atagcgttca
480

taaccttcct ttttaaactg tgatgtgctg gtcagcttgc ccaggtagac ctgtctgtcg
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ggccctcctc catttgatta ctgctggcac ttgctgggta tagcagcaag ccaagcactt
600

cattctcaag agagcatttg gttctgaacc totgttcctt ttgtggacag ctctgatgat
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745

<210> 29
<211> 2127
<212> DNA
<213> Murinae gen. sp.

<400> 29
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120

tccaggagaa cgagatcoga ggactctgcc tgaagtctcg ggagatcttc ctgagtcagc
180

ctatcctttt agaacttgaa gcaccactca agatatgtgg tgacatccac gggcagtact
240

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300

tcggggacta tgtggacagg ggcaagcagt cctggagac aatctgcctc ttgctggcct
360

acaaaatcaa gtatccggag aacttctttc ttctcagagg gaaccacgag tgcgccagca
420

tcaataggat ctacggattt tatgatgagt gtaaaagaag atacaacatt aagctgtgga
480

aaacgttcac agactgtttt aactgcttgc cgatagcagc catcgtggac gagaagatat
540

tctgctgtca tggaggttta tcaccagatc ttcaatctat ggagcagatt cggcgaatta
600

tgagaccaac tgatgtacca gatcaaggtc ttctttgtga tcttttgtgg tctgaccccg
660

ataaagatgt cttaggctgg ggtgaaaatg acagaggagt gtccttcaca tttggtgcag
720

aagtggttgc aaaatttctc cataagcatg atttggatct tatatgtaga gcccatcagg
780

tggttgaaga tggctatgag ttttttgcaa agaggcagtt agtcactctg ttttctgcac
840

ccaactactg tggcgagttt gacaatgcag gcgccatgat gagtgtggat gagaccctca
900

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960

tcacaccacc acgggggtatg atcacaaagc aagcaaagaa atagatgtca cttgacactg
1020

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1080

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1140

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1260

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1380

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1440

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1500

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1560

tcccactgca catttaataa tgattaaagc cattcttttc aatgtctgtg attccttcct
1620

aaagccaaag tttctgttgg actgtatggc acgccctggg gatgagggtg ccagggcatc
1680

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1800

gttcccatat agtctattca ctgagtgatc tttttacagt tggatcaggc ctgaaccggt
1860

ccattcagaa agcttcaa at tatagaaaca acactgtcct atacgagtga ccgataatgc
1920

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1980

aacttgccgt ccaccggttt atacagaact cacagtatct atgacttttt taaactacga
2040

cctgttaa at gaatctgttt gcacagatgc ccgtgtacaa tgccatgtgc tgagaatggt
2100

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2127

<210> 30
<211> 323
<212> PRT
<213> Murinae gen. sp.

<400> 30

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			20					25					30		

Asn	Glu	Ile	Arg	Gly	Leu	Cys	Leu	Lys	Ser	Arg	Glu	Ile	Phe	Leu	Ser
		35					40					45			

Gln	Pro	Ile	Leu	Leu	Glu	Leu	Glu	Ala	Pro	Leu	Lys	Ile	Cys	Gly	Asp
	50					55					60				

Ile	His	Gly	Gln	Tyr	Tyr	Asp	Leu	Leu	Arg	Leu	Phe	Glu	Tyr	Gly	Gly
65					70					75					80

Phe	Pro	Pro	Glu	Ser	Asn	Tyr	Leu	Phe	Leu	Gly	Asp	Tyr	Val	Asp	Arg
				85					90					95	

Gly	Lys	Gln	Ser	Leu	Glu	Thr	Ile	Cys	Leu	Leu	Leu	Ala	Tyr	Lys	Ile
			100					105						110	

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala

115	120	125
Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr 130 135 140		
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro 145 150 155 160		
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu 165 170 175		
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro 180 185 190		
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp 195 200 205		
Pro Asp Lys Asp Val Leu Gly Trp Gly Glu Asn Asp Arg Gly Val Ser 210 215 220		
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp 225 230 235 240		
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu 245 250 255		
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr 260 265 270		
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr 275 280 285		
Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Glu Lys Lys Lys Pro 290 295 300		
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Ala Lys Lys		

<210> 31
 <211> 993
 <212> DNA
 <213> Homo sapiens

<400> 31

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120

aaatcccggg agatTTTTtct gagccagccc attcttcttg agctggaggc acccctcaag
180

atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggc
240

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300

ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg
360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc
420

aagagacgct acaacatcaa actgtggaaa accttactg actgcttcaa ctgcctgccc
480

atcgcggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg
540

cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg
600

ctgtgtgacc tgctgtggtc tgacctgac aaggacgtgc agggctgggg cgagaacgac
660

cgtggcgtct cttttacctt tggagccgag gtgggtggcca agttcctcca caagcacgac
720

ttggacctca tctgccgagc acaccagggtg gtagaagacg gctacgagtt ctttgccaag
780

cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc
840

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900

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<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

<400> 32

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 20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
 35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
 50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
 65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
 85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
 100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
 115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
 130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
 145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
 165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
 180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
 195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
 210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
 225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
 245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
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Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
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<210> 33
<211> 747
<212> DNA
<213> Murinae gen. sp.

<220>
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120

tgcgtatattg ttgagctggg agagtagccc agtggtacag cgcccacctg gaataactga
180

ggacctgggg ttgtctccca gcactgcaaa aggaaaattc actgttacag tcttccttgc
240

acttaaacca gctttgtcta ttgttttttt ggtttggtt tgttactttt gttgctgnnt
300

atTTTTgttg ttgttgtttg tttgtttgag acagggtttt tttgctagcc ctgactgtcc
360

tgaaactccc tctgtagacc aggctggcct caaacttaca gagatccgcc tgcctcagcc
420

tcccaagtgc tgggaataat ggtgtggtca ccaccgccca gccttttgtc tatttttaaa
480

cttgaaagaa acaacagccc agatttcaaa aataatataa tgcacttata cctaaaaaaa
540

caaccaggag tgcccagtta ataacatttt ttaaattgtgg ggatgggaag ggcattagag
600

gagtcttcct tctattgaag attcattaaa gtatttaaga tatgcccttt cactctttat
660

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720

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<210> 34

<211> 2021

<212> DNA

<213> Murinae gen. sp.

<400> 34

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120

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240

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300

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360

ggtgctggca gccattccga cgcttgaaga aaactgtctc gttccccag aagcacatgt
420

atgttacact ggagatgacc aactgatttg tcttataaag gccactgttg agctgggaga
480

gtagcccagt ggtacagcgc ccacctggaa tacttgagga cctgggggttg tctcccagca
540

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600

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660

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720

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780

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840

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900

ccagttaata acacttttta aatgtgggga tgggaagggc attagaggag tcttccttct
960

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1020

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1080

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1200

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1260

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1320

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1380

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1440

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1500

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1560

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1680

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1740

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1800

tgaagggtgct aagacagcgt ctcagtgtg gtcctcotta aggattatct cgccagcgag
1860

gttttcttag atactttgat ccattggag ctctgtttaa gtttaaaatg aaaattatca
1920

tgtactgtat gggaaatgta aatactaact tttccacata tgtaaacttc agacacaaat
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2021

<210> 35
 <211> 709
 <212> PRT
 <213> Murinae gen. sp.

<400> 35

Met Glu Arg Ser Pro Phe Leu Leu Ala Cys Ile Leu Leu Pro Leu Val
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Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
 20 25 30

Met Lys Met Thr Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
 35 40 45

Tyr Asp Gln Gly Ile Ala Ala Val Glu Met Gly His Phe Leu His Leu
 50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Met Phe Leu Cys Gln Ala
 65 70 75 80

Phe Ile Pro Thr Cys Thr Glu Gln Ile His Val Val Leu Pro Cys Arg
 85 90 95

Lys Leu Cys Glu Lys Ile Val Ser Asp Cys Lys Lys Leu Met Asp Thr
 100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asn Arg Leu Pro His
 115 120 125

Cys Asp Asp Thr Val Pro Val Thr Ser His Pro His Thr Glu Leu Ser
 130 135 140

Gly Pro Gln Lys Lys Ser Asp Gln Val Pro Arg Asp Ile Gly Phe Trp
 145 150 155 160

Cys Pro Lys His Leu Arg Thr Ser Gly Asp Gln Gly Tyr Arg Phe Leu
 165 170 175

Gly Ile Glu Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
 180 185 190

Asp Glu Leu Asp Phe Ala Lys Ser Phe Ile Gly Ile Val Ser Ile Phe
 195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
 210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Val Gly Phe Leu Leu Gly Asn
245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
260 265 270

Val Val Leu Gly Ser Lys Asn Lys Ala Cys Ser Val Val Phe Met Phe
275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Ala Pro Gly
325 330 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
420 425 430

Gly Cys Tyr Val Tyr Glu Leu Val Asn Arg Ile Thr Trp Glu Met Thr
435 440 445

Trp Phe Ser Asp His Cys His Gln Tyr Arg Ile Pro Cys Pro Tyr Gln
450 455 460

Ala Asn Pro Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
 465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
 485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
 500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
 515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Gly
 530 535 540

Ala Pro Gly Pro His Arg Leu Lys Val Ile Ser Lys Ser Met Gly Thr
 545 550 555 560

Ser Thr Gly Ala Thr Thr Asn His Gly Thr Ser Ala Met Ala Ile Ala
 565 570 575

Asp His Asp Tyr Leu Gly Gln Glu Thr Ser Thr Glu Val His Thr Ser
 580 585 590

Pro Glu Ala Ser Val Lys Glu Gly Arg Ala Asp Arg Ala Asn Thr Pro
 595 600 605

Ser Ala Lys Asp Arg Asp Cys Gly Glu Ser Ala Gly Pro Ser Ser Lys
 610 615 620

Leu Ser Gly Asn Arg Asn Gly Arg Glu Ser Arg Ala Gly Gly Leu Lys
 625 630 635 640

Glu Arg Ser Asn Gly Ser Glu Gly Ala Pro Ser Glu Gly Arg Val Ser
 645 650 655

Pro Lys Ser Ser Val Pro Glu Thr Gly Leu Ile Asp Cys Ser Thr Ser
 660 665 670

Gln Ala Ala Ser Ser Pro Glu Pro Thr Ser Leu Lys Gly Ser Thr Ser
 675 680 685

Leu Pro Val His Ser Ala Ser Arg Ala Arg Lys Glu Gln Gly Ala Gly
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Ser His Ser Asp Ala
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<210> 36
<211> 2039
<212> DNA
<213> Homo sapiens

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120
cattatttcc ttaaatacatg ttcgacaagt catacaacat gatggccgga accaagaaaa
180
actaaagaaa tttatgattc gaattggagt cttcagcggc ttgtatcttg tgccattagt
240
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300
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360
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420
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720
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780
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gcagggtccc agttcttcag aaccaagcag cctcaaaggt tccacatctc tgcttggtca
1020

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1080

attttctctc gttactcaga agcaaatttg tgttacactg gaagtgacct atgcactggt
1140

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1200

ctggaaaaaa tagagttcaa gaataatatg actcatttca cacaaagggt aatgacaaca
1260

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1320

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1380

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1440

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1500

aacttttttg aaatcctatt caagtatttt tatcatgcta ttgtgatatt ttagcacttt
1560

ggtagctttt acactgaatt tctaagaaaa ttgtaaaata gtcttctttt atactgtaaa
1620

aaaagatata ccaaaaagtc ttataatagg aatttaactt taaaaacca cttattgata
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1740

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1800

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1860

tagtcttttg tatattaggc caagtgcaat tgacttccct tttttaatgt ttcatgacca
1920

ccatttgatt gtattataac cacttacagt tgcttatatt ttttgtttta acttttgttt
1980

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2039

<210> 37
<211> 706
<212> PRT
<213> Homo sapiens

<400> 37

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Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65 70 75 80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
85 90 95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
115 120 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
130 135 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145 150 155 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
165 170 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
180 185 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe
195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp
245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
 260 265 270

Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu
 275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
 290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
 305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly
 325 330 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
 340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
 355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
 370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
 385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
 405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
 420 425 430

Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr
 435 440 445

Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln
 450 455 460

Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
 465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
 485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
 500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
 515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr
 530 535 540

Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr
 545 550 555 560

Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr
 565 570 575

Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser
 580 585 590

Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro
 595 600 605

Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser
 610 615 620

Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly
 625 630 635 640

Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser
 645 650 655

Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro
 660 665 670

Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val
 675 680 685

His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Gly Cys His Ser
 690 695 700

Asp Thr
 705

<210> 38
 <211> 773
 <212> DNA
 <213> Murinae gen. sp.

<400> 38
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120
gttcttttgcc cacaagggtgg agcatgaaag caaggcgcac aatgggagaa gcttccagag
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420
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480
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660
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720
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773

<210> 39
<211> 852
<212> DNA
<213> Murinae gen. sp.

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120
gaatgtgttt tttgccact atgtggagca tgaaagcaat ggcataatg ggagaagctt
180
ccagaggacc gggactcttg cctttgagcg ggtctacact gccaccaga actgcgtaga
240
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300

tgccgccttc gccggactga tgtacctgtt tgtgaggcaa aaatactttg tcggctatct
360

gggagagaga actcagagca cccctggcta catcttcggc aagcggatca tcctgttcct
420

gttcctcatg tccttcgccg ggataactcaa ccattacctc atcttcttct tcggaagcga
480

ctttgagaac tacatcagaa cggtaagcac gacgatctcc ccgctgcttc tcatccctg
540

attgctggag acagagaagg acgctcacca gatcaataga gacgcatcat aacgcaacgc
600

cgccaaggct tctgctctc ttcaagctgt agatgctgtc aatcttgctg ccctcggggc
660

tctgtggcat ccgttaactt tgcttttccg ggaagaaaaa tgtcttgctg tagctccacc
720

cctcgaatgc ggcggtggcc caggatttat tgtctacatc cagcctatac ttctcctggc
780

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840

tagacaaaat tt
852

<210> 40
<211> 161
<212> PRT
<213> Murinae gen. sp.

<400> 40

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Glu Ser Asn Ala His Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
50 55 60

Pro Thr Phe Leu Val Val Leu Trp Thr Ala Gly Leu Leu Cys Ser Gln
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
85 90 95

SUBSTITUTE SHEET (RULE 26)

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
 100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Phe Ala
 115 120 125

Gly Ile Leu Asn His Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
 130 135 140

Asn Tyr Ile Arg Thr Val Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
 145 150 155 160

Pro

<210> 41
 <211> 873
 <212> DNA
 <213> Homo sapiens

<400> 41
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 120

ccctcatcag cgtgggtccag aatggattct ttgcccataa agtggagcac gaaagcagga
 180

cccagaatgg gaggagcttc cagaggaccg gaacacttgc ctttgagcgg gtctacactg
 240

ccaaccagaa ctgtgtagat gcgtaccca ctttcctcgc tgtgctctgg tctgcggggc
 300

tactttgcag ccaagttcct gctgcgtttg ctggactgat gtacttgttt gtgaggcaaa
 360

agtactttgt cggttaccta ggagagagaa cgcagagcac ccctggctac atatttgga
 420

aacgcatcat actcttcctg ttcctcatgt ccgttgctgg catattcaac tattacctca
 480

tcttcttttt cggaagtgac ttgaaaact acataaagac gatctccacc accatctccc
 540

ctctacttct cattocctaa ctctctgctg aatatggggg tggtgttctc atctaataa
 600

tacctacaag tcatcataat tcagctcttg agagcattct gctcttcttt agatggctgt
 660

aaatctattg gccatctggg cttcacagct tgagttaacc ttgcttttcc gggaacaaaa
720

tgatgtcatg tcagctccgc cccttgaaca tgaccgtggc cccaaatttg ctattcccat
780

gcattttgtt tgtttcttca cttatcctgt tctctgaaga tgttttgtga ccaggtttgt
840

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873

<210> 42
<211> 161
<212> PRT
<213> Homo sapiens

<400> 42

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Leu	Ile	Ser	Val	Val	Gln	Asn	Gly	Phe	Phe	Ala	His	Lys	Val	Glu	His
			20					25					30		

Glu	Ser	Arg	Thr	Gln	Asn	Gly	Arg	Ser	Phe	Gln	Arg	Thr	Gly	Thr	Leu
		35					40					45			

Ala	Phe	Glu	Arg	Val	Tyr	Thr	Ala	Asn	Gln	Asn	Cys	Val	Asp	Ala	Tyr
	50					55					60				

Pro	Thr	Phe	Leu	Ala	Val	Leu	Trp	Ser	Ala	Gly	Leu	Leu	Cys	Ser	Gln
65					70					75					80

Val	Pro	Ala	Ala	Phe	Ala	Gly	Leu	Met	Tyr	Leu	Phe	Val	Arg	Gln	Lys
				85					90					95	

Tyr	Phe	Val	Gly	Tyr	Leu	Gly	Glu	Arg	Thr	Gln	Ser	Thr	Pro	Gly	Tyr
			100					105					110		

Ile	Phe	Gly	Lys	Arg	Ile	Ile	Leu	Phe	Leu	Phe	Leu	Met	Ser	Val	Ala
		115					120					125			

Gly	Ile	Phe	Asn	Tyr	Tyr	Leu	Ile	Phe	Phe	Phe	Gly	Ser	Asp	Phe	Glu
	130						135				140				

Asn	Tyr	Ile	Lys	Thr	Ile	Ser	Thr	Thr	Ile	Ser	Pro	Leu	Leu	Leu	Ile
145					150					155					160

Pro

<210> 43
<211> 803
<212> DNA
<213> Murinae gen. sp.

<400> 43
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120
tacggaacac atttcatggt tcctttgaag agttaagaga agaaagtatt tgtaagaaca
180
ggaaaagaaa caaatacttt gcaaataaac tggctgctgc tgtgaccaca tctgaatagc
240
aaaggcgatc gatcaagcgc tgcggacaaa aggcctcctg taagctgcac tgcccgacaa
300
tggttaagctc caatggctcc cagtgccctt atgacgactc ctttaagtac actctgtacg
360
ggtgcatggt cagcatggctc ttcgtgcttg ggctgatatc caactgtggt gcgatataca
420
ttttcatctg tgccctcaaa gtgagaaatg aaactacaac gtacatgatt aacctggcaa
480
tgtcagattt acttttcgtc tttactttgc cttttcggat tttttacttt gcaacacgga
540
attggccatt tggagatcta ctctgtaaga tttcagtaat gctgttttac accaatatgt
600
atgggaagca ttctgttctt aacctgtatc agtgtagatc gatttctggc aattgtctac
660
ccatttaagt caaagacttt aagaaacgaa acgaaaatgc aaagaatcgt ttgcattgcc
720
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803

<210> 44
<211> 1849
<212> DNA
<213> Murinae gen. sp.

<400> 44
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60

cgcgaaacatg cttaggaatt tatctgggat cccttaaacg actgcctatc gccgtccgga
120

atcaatgtag aaatacaaag ttgagaata aaaagaagga agaagtaccc gaggacgacg
180

ggcggacgga cgcacggcga gtgtttgtga ctgaagtaaa gctggtttgg accctggcgg
240

ctgaagcaca agtttccacg cggactggtc tgggccgact tggaacagtt tttccttaca
300

ctttcagctt tatgggttgg cttccttgac tgcattttct gtcagttaac taaactccag
360

actcatggat tttctcgacc agaaaatcag actattttcc tgaataatct actagaaact
420

tttacggaac acatttcatg tttcctttga agagttaaga gaagaaagta tttgtaagaa
480

caggaaaaga aacaaatact ttgcaaataa actggctgct gctgtgacca catctgaata
540

gcaaaggcga tcgatcaagc gctgcggaca aaaggcctcc tgtaagctgc actgcctgac
600

aatggtaagc tccaatggct cccagtgcc ttatgacgac tcctttaagt acactctgta
660

cggggtgcatg ttcagcatgg tcttcgtgct tgggctgata tccaactgtg ttgcgatata
720

cattttcatc tgtgccctca aagtgagaaa tgaaactaca acgtacatga ttaacctggc
780

aatgtcagat ttacttttcg tctttacttt gccatttcgg attttttact ttgcaacacg
840

gaattggcca tttggagatc tactctgtaa gatttcagta atgctgtttt acaccaatat
900

gtatggaagc attctgttct taacctgtat cagtgtagat cgatttctgg caattgtcta
960

cccatttaag tcaaagactt taagaacgaa acgaaatgca aagatcgttt gcattgctgt
1020

gtggttcaca gtgatgggag gaagtgcgcc tgcagttttc tttcagtcga cccactctca
1080

ggggaacaat acctcagaag cctgctttga gaactttcca gcggccacat ggaaaactta
1140

tctctccagg attgtgattt tcattgaaat agtgggcttt tttatccctc tcattttgaa
1200

cgtaacttgt tctagtatgg tgctaagaac tttaaataaa cctgttacat taagtagaag
1260

caaaatgaac aaaactaagg ttttaaaaat gatttttgtc cacttggtca tcttctgttt
1320

ctgttttgtg ccctacaaca tcaacctcat tttgtactcg ctcatgagga cacagacctt
1380

tgtaactgc tctgtggtgg cggcagtga gaccatgtac ccgatcactc tctgcatcgc
1440

tgtttccaac tgctgctttg accctattgt ttactacttc acctcagaca caattcagaa
1500

ctcaataaaa atgaaaaact ggtcgggttag aagaagtga tccaggttct ctgaagttca
1560

gggcactgag aattttatcc aacacaacct acagacctta aaaaataaga tatttgataa
1620

tgaatctgca atataagctg cctgactaag cactgggac tgctccgtgt tcaactgtga
1680

aaactgtgtt cttgggaact atctctccgg ctccaacaga aaatatTTTT aaaggaagtt
1740

tgtgtctgat gtgttaaaca ttaaaatata ttctattctt gtatgcacgc cattttactt
1800

tcttgaacca ctttaacgtg ttttttcctc attaaaaaaaa aaaaactcc
1849

<210> 45

<211> 316

<212> PRT

<213> Murinae gen. sp.

<400> 45

Asp	Asp	Ser	Phe	Lys	Tyr	Thr	Leu	Tyr	Gly	Cys	Met	Phe	Ser	Met	Val
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Phe	Val	Leu	Gly	Leu	Ile	Ser	Asn	Cys	Val	Ala	Ile	Tyr	Ile	Phe	Ile
			20					25					30		

Cys	Ala	Leu	Lys	Val	Arg	Asn	Glu	Thr	Thr	Thr	Tyr	Met	Ile	Asn	Leu
		35					40					45			

Ala	Met	Ser	Asp	Leu	Leu	Phe	Val	Phe	Thr	Leu	Pro	Phe	Arg	Ile	Phe
	50					55					60				

Tyr	Phe	Ala	Thr	Arg	Asn	Trp	Pro	Phe	Gly	Asp	Leu	Leu	Cys	Lys	Ile
65					70					75					80

Ser	Val	Met	Leu	Phe	Tyr	Thr	Asn	Met	Tyr	Gly	Ser	Ile	Leu	Phe	Leu
				85					90					95	

SUBSTITUTE SHEET (RULE 26)

Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys
 100 105 110

Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala Lys Ile Val Cys Ile Ala
 115 120 125

Val Trp Phe Thr Val Met Gly Gly Ser Ala Pro Ala Val Phe Phe Gln
 130 135 140

Ser Thr His Ser Gln Gly Asn Asn Thr Ser Glu Ala Cys Phe Glu Asn
 145 150 155 160

Phe Pro Ala Ala Thr Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe
 165 170 175

Ile Glu Ile Val Gly Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys
 180 185 190

Ser Ser Met Val Leu Arg Thr Leu Asn Lys Pro Val Thr Leu Ser Arg
 195 200 205

Ser Lys Met Asn Lys Thr Lys Val Leu Lys Met Ile Phe Val His Leu
 210 215 220

Val Ile Phe Cys Phe Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu
 225 230 235 240

Tyr Ser Leu Met Arg Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala
 245 250 255

Ala Val Arg Thr Met Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn
 260 265 270

Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln
 275 280 285

Asn Ser Ile Lys Met Lys Asn Trp Ser Val Arg Arg Ser Asp Ser Arg
 290 295 300

Phe Ser Glu Val Gln Gly Thr Glu Asn Phe Ile Gln
 305 310 315

<210> 46
 <211> 1035
 <212> DNA
 <213> Homo sapiens

<400> 46 .

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120

attttcatct gcgtcctcaa agtccgaaat gaaactacaa cttacatgat taacttggca
180

atgtcagact tgctttttgt ttttacttta cccttcagga ttttttactt cacaacacgg
240

aattggccat ttggagattt actttgtaag atttctgtga tgctgtttta taccaacatg
300

tacggaagca ttctgttctt aacctgtatt agtgtagatc gatttctggc aattgtctac
360

ccatttaagt caaagactct aagaaccaa agaatgcaa agattgtttg cactggcgtg
420

tggttaactg tgatcggagg aagtgcaccc gccgtttttg ttcagtctac ccactctcag
480

ggtaacaatg cctcagaagc ctgctttgaa aattttccag aagccacatg gaaaacatat
540

ctctcaagga ttgtaatttt catcgaaata gtgggatttt ttattcctct aattttaaat
600

gtaacttggt ctagtatggg gctaaaaact ttaaccaaac ctgttacatt aagtagaagc
660

aaaataaaca aaactaaggt tttaaaaatg atttttgtac atttgatcat attctgtttc
720

tgttttgttc cttacaatat caatcttatt ttatatctc ttgtgagaac acaaacattt
780

gttaattgct cagtagtggc agcagtaagg acaatgtacc caatcactct ctgtattgct
840

gtttccaact gttgttttga ccctatagtt tactacttta catcggacac aattcagaat
900

tcaataaaaa tgaaaaactg gtctgtcagg agaagtgact tcagattctc tgaagttcat
960

gggtgcagaga atttttattca gcataaccta cagaccttaa aaagtaagat atttgacaat
1020

gaatctgctg cctga
1035

<210> 47

<211> 344

<212> PRT

<213> Homo sapiens

<400> 47

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys
1 5 10 15

Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu
20 25 30

Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val
35 40 45

Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu
50 55 60

Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg
65 70 75 80

Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe
85 90 95

Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val
100 105 110

Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg
115 120 125

Thr Lys Arg Asn Ala Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val
130 135 140

Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln
145 150 155 160

Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr
165 170 175

Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly
180 185 190

Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu
195 200 205

Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys
210 215 220

Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe
225 230 235 240

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Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg
245 250 255

Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met
260 265 270

Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro
275 280 285

Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met
290 295 300

Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His
305 310 315 320

Gly Ala Glu Asn Phe Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys
325 330 335

Ile Phe Asp Asn Glu Ser Ala Ala
340

<210> 48
<211> 814
<212> DNA
<213> Murinae gen. sp.

<400> 48
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ggccaggcct agcacatgta cctcacagac caactggcaa gcagccttca gggagctcga
120

tccccaaaca gccagtcacc acctctgtcc cctctttcact gttgggtcgtc agactgcctg
180

agtggacagc aggctggctg cgttgtatatt tcaacttcctt cctctgactg gcttgctctt
240

gtctctcagt ctttcatccc aggcagctgc ctgaggtagg tgaggaggat ggtgagccag
300

gcagggtctac aataaaggca gctctgtccg gctccttctg gctcgtgagt gtcaccggcc
360

tggaagactg agggaatggc tcccctctct cctccccgtc tttccccagt tccttcctta
420

tgttgggcca tgtgcccagg gagttggaag catcaggag accctcttag tgtggggaag
480

gaagtcagag accattgaca cagtgaagag gcaggatcat gtgttggaag cctgttagca
540

ggaccaaggt gactcttggg agagactctt gtggacacag gccgtggtgg cttgtcagac
600

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660

gggacactgc tgagtaatga gcagcttatt acacacaatg ggaagagggg cagagagggc
720

tgtgtcgggt gagtctcggc tgggactgaa gtttgccata agtagtggtt gtacatccag
780

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814

<210> 49
<211> 1164
<212> DNA
<213> Murinae gen. sp.

<400> 49
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120

cagcccagcc tcttgggggt caggagggtc ctgcagaaac tccagacgga cggactcaag
180

gagtgcatta tcttctgcgt gcgggaggag cctgtggtgt tcttgcgcg tgaggaggac
240

tttgtgtctt acacacctcg agacaaggag agccttcatt agaacctcag ggacctagt
300

ccaggggtca aggctgagaa tctggagctg gccatccaga aagagatcca tgactttgcc
360

caattgagag ataatgtgta ccacgtatac cacaacacag aggacctgcg cggggagccg
420

cacaccgtgg ccatccgagg tgaggatggc gtgtgcgtga ccgaggaggt gtttaagcgg
480

ccgtctttcc tgcagccac ctacagatac caccgcctcc ccttgccaga gcaaggggcc
540

cccctggaag ccagtttga tgcctttgtc agcgttcttc gggagacccc cagccttctg
600

ccactcagag ataaccacgg gcctctgcct gccctcctgt tcagctgcca gtcagggtga
660

ggcagaacca acctaggcat ggtcctggga accctcgtca tgttccacca cagtaggacc
720

acctcccagc tagaggcagc ctccccgttg gccaaacccc tgcccatgga gcagtttcag
780

gtgatccagg gcttcatctg taagggtgcca caggggaaga aaatgggtgga ggaggtggat
840

cgagcgatca gtgcctgtgc agagttgcat gacctgaagg aggaggtcct aaaaaaccag
900

aggaggctgg aaagcttcag gccagagagc cggggacagg aatgtggttag tcagcaagct
960

gtccagcaga gggcgctgtg gagcctggag ctgtacttct atctgctcct atttaactac
1020

tatctgcatg agcagtaccc cctggccttt gccctcagtt tcagtcgatg gctgtgtacc
1080

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1140

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<210> 50

<211> 388

<212> PRT

<213> Murinae gen. sp.

<400> 50

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Gly	Thr	Leu	Lys	Ser	Cys	Gly	Ala	Pro	Asn	Phe	Arg	Gln	Val	Arg	Gly
		20						25					30		

Gly	Leu	Pro	Val	Phe	Gly	Met	Gly	Gln	Pro	Ser	Leu	Leu	Gly	Phe	Arg
		35					40					45			

Arg	Val	Leu	Gln	Lys	Leu	Gln	Thr	Asp	Gly	Leu	Lys	Glu	Cys	Ile	Ile
	50					55					60				

Phe	Cys	Val	Arg	Glu	Glu	Pro	Val	Val	Phe	Leu	Arg	Ala	Glu	Glu	Asp
65					70					75					80

Phe	Val	Ser	Tyr	Thr	Pro	Arg	Asp	Lys	Glu	Ser	Leu	His	Glu	Asn	Leu
				85					90					95	

Arg	Asp	Pro	Ser	Pro	Gly	Val	Lys	Ala	Glu	Asn	Leu	Glu	Leu	Ala	Ile
			100					105					110		

Gln Lys Glu Ile His Asp Phe Ala Gln Leu Arg Asp Asn Val Tyr His

115	120	125
Val Tyr His Asn Thr Glu Asp Leu Arg Gly Glu Pro His Thr Val Ala 130 135 140		
Ile Arg Gly Glu Asp Gly Val Cys Val Thr Glu Glu Val Phe Lys Arg 145 150 155 160		
Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg Leu Pro Leu Pro 165 170 175		
Glu Gln Gly Ala Pro Leu Glu Ala Gln Phe Asp Ala Phe Val Ser Val 180 185 190		
Leu Arg Glu Thr Pro Ser Leu Leu Pro Leu Arg Asp Asn His Gly Pro 195 200 205		
Leu Pro Ala Leu Leu Phe Ser Cys Gln Ser Gly Val Gly Arg Thr Asn 210 215 220		
Leu Gly Met Val Leu Gly Thr Leu Val Met Phe His His Ser Arg Thr 225 230 235 240		
Thr Ser Gln Leu Glu Ala Ala Ser Pro Leu Ala Lys Pro Leu Pro Met 245 250 255		
Glu Gln Phe Gln Val Ile Gln Gly Phe Ile Cys Lys Val Pro Gln Gly 260 265 270		
Lys Lys Met Val Glu Glu Val Asp Arg Ala Ile Ser Ala Cys Ala Glu 275 280 285		
Leu His Asp Leu Lys Glu Glu Val Leu Lys Asn Gln Arg Arg Leu Glu 290 295 300		
Ser Phe Arg Pro Glu Ser Arg Gly Gln Glu Cys Gly Ser Gln Gln Ala 305 310 315 320		
Val Gln Gln Arg Ala Leu Trp Ser Leu Glu Leu Tyr Phe Tyr Leu Leu 325 330 335		
Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu Ala Phe Ala Leu 340 345 350		
Ser Phe Ser Arg Trp Leu Cys Thr His Pro Glu Leu Tyr Arg Leu Leu 355 360 365		

Val Glu Leu Asn Ser Val Gly Pro Leu Val Pro Gly Asp Leu Ile Ala
370 375 380

Lys Gly Ser Leu
385

<210> 51
<211> 4303
<212> DNA
<213> Homo sapiens

<400> 51
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120

cactccttcc agagcactag cttgcataac agcaaggcca agtccatcat cccaacaag
180

gtggcccctg ttgtgatcac gtacaactgc aaggaggagt tccagatcca tgatgagctg
240

ctcaaggctc attacacgtt gggccggctc tcggacaaca ccctgagca ctacctggtg
300

caaggccgct acttcctggt gcgggatgtc actgagaaga tggatgtgct gggcaccgtg
360

ggaagctgtg gggcccccaa ctcccggcag gtgcagggtg ggctcactgt gttcggcatg
420

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480

agggagtgtg tcattctctg tgtgcgggag gaacctgtgc ttttcctgcg tgcagatgag
540

gactttgtgt cctacacacc tcgagacaag cagaaccttc atgagaacct ccagggcctt
600

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660

gcccagctga gcgagaacac ataccatgtg taccataaca ccgaggacct gtgggggggag
720

cccatgctg tggccatcca tggtagaggac gacttgcattg tgacggagga ggtgtacaag
780

cggcccctct tcctgcagcc cacctacagg taccaccgcc tgcccctgcc cgagcaaggg
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agtcccctgg agggccagtt ggacgccttt gtcagtgttc tccgggagac cccagcctg
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ctgcagctcc gtgatgccca cgggcctccc ccagccctcg tcttcagctg ccagatgggc
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gtgggcagga ccaacctggg catggtcctg ggcacctca tcttgcttca ccgcagtggg
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accacctccc agccagaggc tgccccacg caggccaagc ccctgcctat ggagcagttc
1080

caggtgatcc agagctttct ccgcatgggtg cccagggaa ggaggatggg ggaagagggtg
1140

gacagagcca tcttgctg tgccgagttg catgacctga aagaagtggg cttggaaaac
1200

cagaagaagt tagaaggat ccgaccggag agcccagccc aggggaagcgg cagccgacac
1260

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1440

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ggcacggccc agcccagcgc caaggccctg gggagcatcc tggcctacct gacggacgcc
1620

aagaggaggc tgcggaagggt tgtctgggtg agccttcggg aggaggccgt gttggagtgt
1680

gacgggcaca cctacagcct gcggtggcct gggccccctg tggctcctga ccagctggag
1740

accctggagg cccagctgaa ggcccatcta agcgagcctc cccagggcaa ggaggggccc
1800

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Asp Ser Arg His Ser Val Ser Ile His Ser Phe Gln Ser Thr Ser Leu
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His Asn Ser Lys Ala Lys Ser Ile Ile Pro Asn Lys Val Ala Pro Val
 50 55 60

Val Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu
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Leu Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu
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His Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu
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Lys Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe
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Arg Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser
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Leu Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His
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Arg Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu
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Arg Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn
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Leu His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser
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Leu Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser
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Glu Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu
 225 230 235 240

Pro His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu
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Glu Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His
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Asp Ala His Gly Pro Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly
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Val Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu
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His Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala
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Lys Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg
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Met Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile
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Thr Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn
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Gln Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser
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Gly Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg
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Tyr Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro
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Pro Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg
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Arg Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys
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Ala Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu
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Pro Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys
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Leu Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly
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Gly Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala
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Lys Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu
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Leu Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp
 725 730 735

Thr Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile

740	745	750
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Cys Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser 785 790 795 800		
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Gly Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser 820 825 830		
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